

0580  
12/2

#2

OPIE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/997,900

DATE: 12/07/2001  
 TIME: 12:49:59

Input Set : A:\2411481.app  
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3 <110> APPLICANT: Kakefuda, Genichi  
 4 Costello, Colleen  
 5 Sun, Ming  
 6 Hu, Weiming  
 8 <120> TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance  
 9 in Plants  
 11 <130> FILE REFERENCE: 043753/241148 (5849-20A)  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/997,900  
 C--> 14 <141> CURRENT FILING DATE: 2001-11-30  
 16 <150> PRIOR APPLICATION NUMBER: 60/106,239  
 17 <151> PRIOR FILING DATE: 1998-10-29  
 19 <150> PRIOR APPLICATION NUMBER: 09/426,568  
 20 <151> PRIOR FILING DATE: 1999-10-22  
 22 <160> NUMBER OF SEQ ID NOS: 11  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1673  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Arabidopsis sp.  
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 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (42)..(1514)  
 34 <223> OTHER INFORMATION: Mature Peptide  
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 38 Met Ala Ala Ile Ser  
 39 1 5  
 41 gta agt tct tca cca tct att cgc tgc ttg aga tcg gca tgt tcc gat 104  
 42 Val Ser Ser Ser Pro Ser Ile Arg Cys Leu Arg Ser Ala Cys Ser Asp  
 43 10 15 20  
 45 tct tct cct gct ctt gta tcc tcg acg cgt gta tcg ttc ccg gcg aag 152  
 46 Ser Ser Pro Ala Leu Val Ser Ser Thr Arg Val Ser Phe Pro Ala Lys  
 47 25 30 35  
 49 att tca tat ctc tcc ggt ata tct tcg cac cgt ggc gat gaa atg ggt 200  
 50 Ile Ser Tyr Leu Ser Gly Ile Ser Ser His Arg Gly Asp Glu Met Gly  
 51 40 45 50  
 53 aag aga atg gaa gga ttc gtt aga agc gtc gat ggg aag atc tct gat 248  
 54 Lys Arg Met Glu Gly Phe Val Arg Ser Val Asp Gly Lys Ile Ser Asp  
 55 55 60 65  
 57 gcg tct ttc tcc gaa gct tca tct gcg act cca aaa tcg aag gtg agg 296  
 58 Ala Ser Phe Ser Glu Ala Ser Ser Ala Thr Pro Lys Ser Lys Val Arg  
 59 70 75 80 85  
 61 aag cac aca att tca gta ttt gtt gga gac gaa agc gga atg att aat 344  
 62 Lys His Thr Ile Ser Val Phe Val Gly Asp Glu Ser Gly Met Ile Asn  
 63 90 95 100  
 65 agg att gca gga gtg ttt gca agg aga gga tac aat att gag agt ctt 392  
 66 Arg Ile Ala Gly Val Phe Ala Arg Arg Gly Tyr Asn Ile Glu Ser Leu

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67          105          110          115
69 gct gtt ggt ctg aac aga gac aag gct cta ttc acc ata gtt gtc tgt 440
70 Ala Val Gly Leu Asn Arg Asp Lys Ala Leu Phe Thr Ile Val Val Cys
71          120          125          130
73 gga act gaa agg gta ctt cag cag gtc atc gag caa ctc cag aag ctc 488
74 Gly Thr Glu Arg Val Leu Gln Gln Val Ile Glu Gln Leu Gln Lys Leu
75          135          140          145
77 gtt aat gtt cta aag gtt gaa gat atc tca agt gag ccg caa gtg gag 536
78 Val Asn Val Leu Lys Val Glu Asp Ile Ser Ser Glu Pro Gln Val Glu
79 150          155          160          165
81 cgt gag ctg atg ctt gta aaa gtg aat gca cat cca gaa tcc agg gca 584
82 Arg Glu Leu Met Leu Val Lys Val Asn Ala His Pro Glu Ser Arg Ala
83          170          175          180
85 gag atc atg tgg cta gtt gac aca ttc aga gca aga gtt gta gat ata 632
86 Glu Ile Met Trp Leu Val Asp Thr Phe Arg Ala Arg Val Val Asp Ile
87          185          190          195
89 gcg gaa cat gca ttg act atc gag gta act gga gat cct gga aaa atg 680
90 Ala Glu His Ala Leu Thr Ile Glu Val Thr Gly Asp Pro Gly Lys Met
91          200          205          210
93 att gct gta gaa aga aat ttg aaa aag ttt cag atc aga gag att gta 728
94 Ile Ala Val Glu Arg Asn Leu Lys Lys Phe Gln Ile Arg Glu Ile Val
95          215          220          225
97 agg aca gga aag ata gca ctg aga agg gaa aag atg ggt gca act gct 776
98 Arg Thr Gly Lys Ile Ala Leu Arg Arg Glu Lys Met Gly Ala Thr Ala
99 230          235          240          245
101 cca ttt tgg cga ttt tca gca gca tcc tat cca gat ctc aag gag caa 824
102 Pro Phe Trp Arg Phe Ser Ala Ala Ser Tyr Pro Asp Leu Lys Glu Gln
103          250          255          260
105 gcg cct gtt agt gtt ctt cga agt agc aaa aaa gga gcc att gtc cct 872
106 Ala Pro Val Ser Val Leu Arg Ser Ser Lys Lys Gly Ala Ile Val Pro
107          265          270          275
109 caa aag gaa aca tca gca ggg gga gat gtt tat ccc gtt gag cca ttt 920
110 Gln Lys Glu Thr Ser Ala Gly Gly Asp Val Tyr Pro Val Glu Pro Phe
111          280          285          290
113 ttt gac ccc aag gta cat cgt att ctc gac gct cac tgg gga ctt ctc 968
114 Phe Asp Pro Lys Val His Arg Ile Leu Asp Ala His Trp Gly Leu Leu
115          295          300          305
117 act gac gaa gat acg agt gga cta cgg tcg cat act cta tca ttg ctt 1016
118 Thr Asp Glu Asp Thr Ser Gly Leu Arg Ser His Thr Leu Ser Leu Leu
119 310          315          320          325
121 gta aat gat att cca gga gtt ctt aat att gtg act ggt gtt ttc gct 1064
122 Val Asn Asp Ile Pro Gly Val Leu Asn Ile Val Thr Gly Val Phe Ala
123          330          335          340
125 cga agg gga tac aat atc cag agc ttg gcc gta gga cat gct gaa acc 1112
126 Arg Arg Gly Tyr Asn Ile Gln Ser Leu Ala Val Gly His Ala Glu Thr
127          345          350          355
129 aag ggc att tca cgc att aca aca gtt ata cct gca aca gat gaa tcg 1160
130 Lys Gly Ile Ser Arg Ile Thr Thr Val Ile Pro Ala Thr Asp Glu Ser
131          360          365          370

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133 gtc agc aaa ttg gtg cag caa ctt tac aaa ctc gta gat gtg cat gag 1208
134 Val Ser Lys Leu Val Gln Gln Leu Tyr Lys Leu Val Asp Val His Glu
135      375      380      385
137 gtc cat gat ctt act cat ttg cca ttt tct gaa aga gaa ctg atg ctg 1256
138 Val His Asp Leu Thr His Leu Pro Phe Ser Glu Arg Glu Leu Met Leu
139 390      395      400      405
141 att aag att gcc gtg aac gct gct gct aga aga gat gtc ctg gac att 1304
142 Ile Lys Ile Ala Val Asn Ala Ala Ala Arg Asp Val Leu Asp Ile
143      410      415      420
145 gct agt att ttc agg gct aaa gct gtt gac gta tct gat cac aca att 1352
146 Ala Ser Ile Phe Arg Ala Lys Ala Val Asp Val Ser Asp His Thr Ile
147      425      430      435
149 act ttg cag ctt act ggg gat cta gac aag atg gtt gca ctg caa agg 1400
150 Thr Leu Gln Leu Thr Gly Asp Leu Asp Lys Met Val Ala Leu Gln Arg
151      440      445      450
153 tta ttg gag ccc tat ggt ata tgt gag gtt gca aga acc ggt cgt gtg 1448
154 Leu Leu Glu Pro Tyr Gly Ile Cys Glu Val Ala Arg Thr Gly Arg Val
155      455      460      465
157 gca ttg gct cgt gaa tcg gga gtg gac tcc aag tac ctt cgt gga tac 1496
158 Ala Leu Ala Arg Glu Ser Gly Val Asp Ser Lys Tyr Leu Arg Gly Tyr
159 470      475      480      485
161 tcc ttt ctt tta aca ggc taaaccgttg cagagtgcac ccacgaaca 1544
162 Ser Phe Leu Leu Thr Gly
163      490
165 tcagaaactt tggaaggtaa aagtttcatt acacagtcta tgaacctcaa agacagacag 1604
167 agagactgcg togatatatg ttgtgactt tgtttatgaa acaattagct gattttgggc 1664
169 ttcatttcg 1673
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173 <211> LENGTH: 491
174 <212> TYPE: PRT
175 <213> ORGANISM: Arabidopsis sp.
177 <400> SEQUENCE: 2
178 Met Ala Ala Ile Ser Val Ser Ser Ser Pro Ser Ile Arg Cys Leu Arg
179 1      5      10      15
181 Ser Ala Cys Ser Asp Ser Ser Pro Ala Leu Val Ser Ser Thr Arg Val
182      20      25      30
184 Ser Phe Pro Ala Lys Ile Ser Tyr Leu Ser Gly Ile Ser Ser His Arg
185      35      40      45
187 Gly Asp Glu Met Gly Lys Arg Met Glu Gly Phe Val Arg Ser Val Asp
188      50      55      60
190 Gly Lys Ile Ser Asp Ala Ser Phe Ser Glu Ala Ser Ser Ala Thr Pro
191 65      70      75      80
193 Lys Ser Lys Val Arg Lys His Thr Ile Ser Val Phe Val Gly Asp Glu
194      85      90      95
196 Ser Gly Met Ile Asn Arg Ile Ala Gly Val Phe Ala Arg Arg Gly Tyr
197      100      105      110
199 Asn Ile Glu Ser Leu Ala Val Gly Leu Asn Arg Asp Lys Ala Leu Phe
200      115      120      125
202 Thr Ile Val Val Cys Gly Thr Glu Arg Val Leu Gln Gln Val Ile Glu

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203      130      135      140
205 Gln Leu Gln Lys Leu Val Asn Val Leu Lys Val Glu Asp Ile Ser Ser
206 145      150      155      160
208 Glu Pro Gln Val Glu Arg Glu Leu Met Leu Val Lys Val Asn Ala His
209      165      170      175
211 Pro Glu Ser Arg Ala Glu Ile Met Trp Leu Val Asp Thr Phe Arg Ala
212      180      185      190
214 Arg Val Val Asp Ile Ala Glu His Ala Leu Thr Ile Glu Val Thr Gly
215      195      200      205
217 Asp Pro Gly Lys Met Ile Ala Val Glu Arg Asn Leu Lys Lys Phe Gln
218 210      215      220
220 Ile Arg Glu Ile Val Arg Thr Gly Lys Ile Ala Leu Arg Arg Glu Lys
221 225      230      235      240
223 Met Gly Ala Thr Ala Pro Phe Trp Arg Phe Ser Ala Ala Ser Tyr Pro
224      245      250      255
226 Asp Leu Lys Glu Gln Ala Pro Val Ser Val Leu Arg Ser Ser Lys Lys
227      260      265      270
229 Gly Ala Ile Val Pro Gln Lys Glu Thr Ser Ala Gly Gly Asp Val Tyr
230      275      280      285
232 Pro Val Glu Pro Phe Phe Asp Pro Lys Val His Arg Ile Leu Asp Ala
233 290      295      300
235 His Trp Gly Leu Leu Thr Asp Glu Asp Thr Ser Gly Leu Arg Ser His
236 305      310      315      320
238 Thr Leu Ser Leu Leu Val Asn Asp Ile Pro Gly Val Leu Asn Ile Val
239      325      330      335
241 Thr Gly Val Phe Ala Arg Arg Gly Tyr Asn Ile Gln Ser Leu Ala Val
242      340      345      350
244 Gly His Ala Glu Thr Lys Gly Ile Ser Arg Ile Thr Thr Val Ile Pro
245      355      360      365
247 Ala Thr Asp Glu Ser Val Ser Lys Leu Val Gln Gln Leu Tyr Lys Leu
248      370      375      380
250 Val Asp Val His Glu Val His Asp Leu Thr His Leu Pro Phe Ser Glu
251 385      390      395      400
253 Arg Glu Leu Met Leu Ile Lys Ile Ala Val Asn Ala Ala Ala Arg Arg
254      405      410      415
256 Asp Val Leu Asp Ile Ala Ser Ile Phe Arg Ala Lys Ala Val Asp Val
257      420      425      430
259 Ser Asp His Thr Ile Thr Leu Gln Leu Thr Gly Asp Leu Asp Lys Met
260      435      440      445
262 Val Ala Leu Gln Arg Leu Leu Glu Pro Tyr Gly Ile Cys Glu Val Ala
263 450      455      460
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266 465      470      475      480
268 Tyr Leu Arg Gly Tyr Ser Phe Leu Leu Thr Gly
269      485      490
273 <210> SEQ ID NO: 3
274 <211> LENGTH: 4895
275 <212> TYPE: DNA
276 <213> ORGANISM: Arabidopsis sp.

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279 <221> NAME/KEY: promoter
280 <222> LOCATION: (1)..(757)
281 <223> OTHER INFORMATION: Promoter Region
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285 <222> LOCATION: (717)
286 <223> OTHER INFORMATION: Transcriptional Starting Point
288 <220> FEATURE:
289 <221> NAME/KEY: misc_signal
290 <222> LOCATION: (758)..(760)
291 <223> OTHER INFORMATION: Start Codon
293 <220> FEATURE:
294 <221> NAME/KEY: misc_signal
295 <222> LOCATION: (4737)..(4739)
296 <223> OTHER INFORMATION: Stop Codon
298 <220> FEATURE:
299 <223> OTHER INFORMATION: n at position 694 can be a, c, g, or t
301 <400> SEQUENCE: 3
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303 acgacgaagc gatccagttg agaattgtct cgagattcct cgttttagct gtcccactac 120
304 attcgcgatg atttcgaaat ctctttctct tcttctctct ttcgtcttct tctgcgaaaa 180
305 aatcgaatgg ataatacat tttctttttc tcgagaaaaa tgatctggtg attatgtgag 240
306 atccgtctct agcgcgttgc ttatcgagaa ataattaatt ttaatttgac gggatgaagat 300
307 attattggcg acgtctgttt ccgattgact ttgatttgac ttttcctttc aatcattatt 360
308 tggcgagtcc cgcgtaaaata tggactcttc ttgattgtcc cacttttttc ggtggcttta 420
309 ccggatttaa aatcattttc ttttctctaa ttatgaattt taccctaaac ttctcataat 480
310 tacaattagt tccgacgaac ccaagatact ttttagcaaa attaggaaaa tagttgactc 540
311 gaaaagggtt ttataacgtg gagctgacgt gttgggttta tctactcgaa gccttttggg 600
312 cttttcttaa agccattgat ttctaaggtc gtcaacaacc gaaccggacc ggacggtttg 660
W--> 313 accggtctaa ccaacatata tacgttcttt ttcnacttgc cgtttcgtcg tcgtcagttc 720
314 tcttcagtag caaaaaacct tcggtctcgt ctcgtaaatg gcggccattt ctgtaagttc 780
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321 gattgcagga gtgtttgcaa ggagaggata caatattgag agtcttgctg ttggtctgaa 1200
322 cagagacaag gctctattca ccatagttgt ctgtggaact gaaagggtac ttcagcaggt 1260
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327 gtaaaagtga atgcacatcc agaatccagg gcagaggtac tattccttgc ctatgggaaa 1560
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329 tctctaaaatt tgattaagct tctgttttaa tgaattcaca gatcatgtgg ctagttgaca 1680
330 cattcagagc aagagttgta gatatagcgg aacatgcatt gactatcgag gtacatctac 1740
331 ttattatgat ttgtgttggg cttgatattt gtttcgcact gtagcctgtg gggttcaaga 1800

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VERIFICATION SUMMARY

DATE: 12/07/2001

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Input Set : A:\2411481.app

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3